FIG. 1A

```
    GTCCTTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTTCTCTGCTCGCCGCTG
  1 ---------+---------+---------+---------+---------+---------+ 60
    CAGGAAGGTGGTACGTGAGCGACCCGAAGAAGAGACACCGCACAAGAGACGAGCGGCGAC
C             M  H  S  L  G  F  F  S  V  A  C  S  L  L  A  A  A -

    CGCTGCTCCCGGGTCCTCGCGAGGCGCCCGCCGCCGCCGCCTTCGAGTCCGGACTCG
 61 ---------+---------+---------+---------+---------+---------+ 120
    GCGACGAGGGCCCAGGAGCGCTCCGCGGGCGGCGGCGGCGGAAGCTCAGGCCTGAGC
C     L  L  P  G  P  R  E  A  P  A  A  A  A  A  F  E  S  G  L  D -

    ACCTCTCGGACGCGGAGCCCGACGCGGGCGAGGCCACGGCTTATGCAAGCAAAGATCTGG
121 ---------+---------+---------+---------+---------+---------+ 180
    TGGAGAGCCTGCGCCTCGGGCTGCGCCCGCTCCGGTGCCGAATACGTTCGTTTCTAGACC
C     L  S  D  A  E  P  D  A  G  E  A  T  A  Y  A  S  K  D  L  E -

    AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACTCATGACTGTACTCTACCCAGAAT
181 ---------+---------+---------+---------+---------+---------+ 240
    TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA
C     E  Q  L  R  S  V  S  S  V  D  E  L  M  T  V  L  Y  P  E  Y -

    ATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG
241 ---------+---------+---------+---------+---------+---------+ 300
    TAACCTTTTACATGTTCACAGTCGATTCCTTTCCTCCGACCGTTGTATTGTCTCTTGTCC
C     W  K  M  Y  K  C  Q  L  R  K  G  G  W  Q  H  N  R  E  Q  A -

    CCAACCTCAACTCAAGGACAGAAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG
```

MATCH WITH FIG. 1B

FIG. 1B

MATCH WITH FIG. 1A

```
    301 ---------+---------+---------+---------+---------+---------+ 360
        GGTTGGAGTTGAGTTCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATTATGTC
C        N  L  N  S  R  T  E  E  T  I  K  F  A  A  A  H  Y  N  T  E -

        AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
    361 ---------+---------+---------+---------+---------+---------+ 420
        TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
C        I  L  K  S  I  D  N  E  W  R  K  T  Q  C  M  P  R  E  V  C -

        GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
    421 ---------+---------+---------+---------+---------+---------+ 480
        CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC
C        I  D  V  G  K  E  F  G  V  A  T  N  T  F  F  K  P  P  C  V -

        TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
    481 ---------+---------+---------+---------+---------+---------+ 540
        ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT
C        S  V  Y  R  C  G  G  C  C  N  S  E  G  L  Q  C  M  N  T  S -

        GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCA
    541 ---------+---------+---------+---------+---------+---------+ 600
        CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGGT
C        T  S  Y  L  S  K  T  L  F  E  I  T  V  P  L  S  Q  G  P  K -

        AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
    601 ---------+---------+---------+---------+---------+---------+ 660
        TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTAC
C        P  V  T  I  S  F  A  N  H  T  S  C  R  C  M  S  K  L  D  V -
```

MATCH WITH FIG. 1C

MATCH WITH FIG. 1B

FIG. 1C

```
     TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
661  ---------+---------+---------+---------+---------+---------+ 720
     AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGTGATGGTGTCACAG
C     Y  R  Q  V  H  S  I  I  R  R  S  L  P  A  T  L  P  Q  C  Q -

     AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
721  ---------+---------+---------+---------+---------+---------+ 780
     TCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGG
C     A  A  N  K  T  C  P  T  N  Y  M  W  N  N  H  I  C  R  C  L -

     TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
781  ---------+---------+---------+---------+---------+---------+ 840
     ACCGAGTCCTTCTAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
C     A  Q  E  D  F  M  F  S  S  D  A  G  D  D  S  T  D  G  F  H -

     ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG
841  ---------+---------+---------+---------+---------+---------+ 900
     TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
C     D  I  C  G  P  N  K  E  L  D  E  E  T  C  Q  C  V  C  R  A -

     CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT
901  ---------+---------+---------+---------+---------+---------+ 960
     GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTTCTTGATCTGTCTTTGAGTACGGTCA
C     G  L  R  P  A  S  C  G  P  H  K  E  L  D  R  N  S  C  Q  C -

     GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA
961  ---------+---------+---------+---------+---------+---------+ 1020
     CACAGACATTTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
```

MATCH WITH FIG. 1D

FIG. 1D

MATCH WITH FIG. 1C

```
C       V  C  K  N  K  L  F  P  S  Q  C  G  A  N  R  E  F  D  E  N -

        ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
1021    ----+----+---------+---------+---------+---------+---------+---------+ 1080
        TGTGTACGGTCACACATACATTTTCTTGGACGGGGTCTTTAGTTGGGGATTTAGGACCTT
C       T  C  Q  C  V  C  K  R  T  C  P  R  N  Q  P  L  N  P  G  K -

        AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC
1081    ---------+---------+---------+---------+---------+---------+---------+ 1140
        TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTTCTTCAAGG
C       C  A  C  E  C  T  E  S  P  Q  K  C  L  L  K  G  K  K  F  H -

        ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC
1141    ---------+---------+---------+---------+---------+---------+---------+ 1200
        TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
C       H  Q  T  C  S  C  Y  R  R  P  C  T  N  R  Q  K  A  C  E  P -

        CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC
1201    ---------+---------+---------+---------+---------+---------+---------+ 1260
        GTCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
C       G  F  S  Y  S  E  E  V  C  R  C  V  P  S  Y  W  Q  R  P  Q -

        AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT
```

MATCH WITH FIG. 1E

MATCH WITH FIG. 1D

FIG. 1E

```
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
C      M  S  *

     TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT

     AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC

     CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC
1441 ---------+---------+---------+---------+---------+---------+ 1500
     GTTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCGGTTCTAAAAGGAG

     TTGTGATTTCTTTAAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC
1501 ---------+---------+---------+---------+---------+---------+ 1560
     AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTTATAACAAAGACG

     ATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
     TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA

     GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAAAAAAAAAAAA
1621 -- ------+---------+---------+---------+---------+---- 1674
     CGTTTTATACAAATTTTATTTTACTTTTAACATAAATATTTTTTTTTTTTTTTT
```

```
  1  CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
     ---------+---------+---------+---------+---------+---------+

 71  AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAAAATGTACAAGTGTCAGCTAAG
     ---------+---------+---------+---------+---------+---------+
                 M  T  V  L  Y  P  E  Y  W  K  M  Y  K  C  Q  L  R

121  GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
     ---------+---------+---------+---------+---------+---------+
      K  G  G  W  Q  H  N  R  E  Q  A  N  L  N  S  R  T  E  E  T

181  TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
     ---------+---------+---------+---------+---------+---------+
      I  K  F  A  A  A  H  Y  N  T  E  I  L  K  S  I  D  N  E  W

241  GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
     ---------+---------+---------+---------+---------+---------+
      R  K  T  Q  C  M  P  R  E  V  C  I  D  V  G  K  E  F  G  V

301  CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGTTGCTG
     ---------+---------+---------+---------+---------+---------+
      A  T  N  T  F  F  K  P  P  C  V  S  V  Y  R  C  G  G  C  C
```

FIG. 2A

```
361  CAATAGTGAGGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATT
     ---------+---------+---------+---------+---------+---------+
      N  S  E  G  L  Q  C  M  N  T  S  T  S  Y  L  S  K  T  L  F

421  TGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCA
     ---------+---------+---------+---------+---------+---------+
      E  I  T  V  P  L  S  Q  G  P  K  P  V  T  I  S  F  A  N  H

481  CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
     ---------+---------+---------+---------+---------+---------+
      T  S  C  R  C  M  S  K  L  D  V  Y  R  Q  V  H  S  I  I  R

541  ACGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAA
     ---------+---------+---------+---------+---------+---------+
      R  S  L  P  A  T  L  P  Q  C  Q  A  A  N  K  T  C  P  T  N

601  TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTC
     ---------+---------+---------+---------+---------+---------+
      Y  M  W  N  N  H  I  C  R  C  L  A  Q  E  D  F  M  F  S  S

661  GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
     ---------+---------+---------+---------+---------+---------+
      D  A  G  D  D  S  T  D  G  F  H  D  I  C  G  P  N  K  E  L
```

FIG.2B

```
721  GGATGAAGAGACCTGTCAGTGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACC
     ---------+---------+---------+---------+---------+---------+
      D  E  E  T  C  Q  C  V  C  R  A  G  L  R  P  A  S  C  G  P

781  CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAAACTCTTCCCCAG
     ---------+---------+---------+---------+---------+---------+
      H  K  E  L  D  R  N  S  C  Q  C  V  C  K  N  K  L  F  P  S

841  CCAATGTGGGGCCAACCGAGAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAAC
     ---------+---------+---------+---------+---------+---------+
      Q  C  G  A  N  R  E  F  D  E  N  T  C  Q  C  V  C  K  R  T

901  CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCC
     ---------+---------+---------+---------+---------+---------+
      C  P  R  N  Q  P  L  N  P  G  K  C  A  C  E  C  T  E  S  P

961  ACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACG
     ---------+---------+---------+---------+---------+---------+
      Q  K  C  L  L  K  G  K  K  F  H  H  Q  T  C  S  C  Y  R  R

1021 GCCATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
     ---------+---------+---------+---------+---------+---------+
      P  C  T  N  R  Q  K  A  C  E  P  G  F  S  Y  S  E  E  V  C
```

FIG. 2C

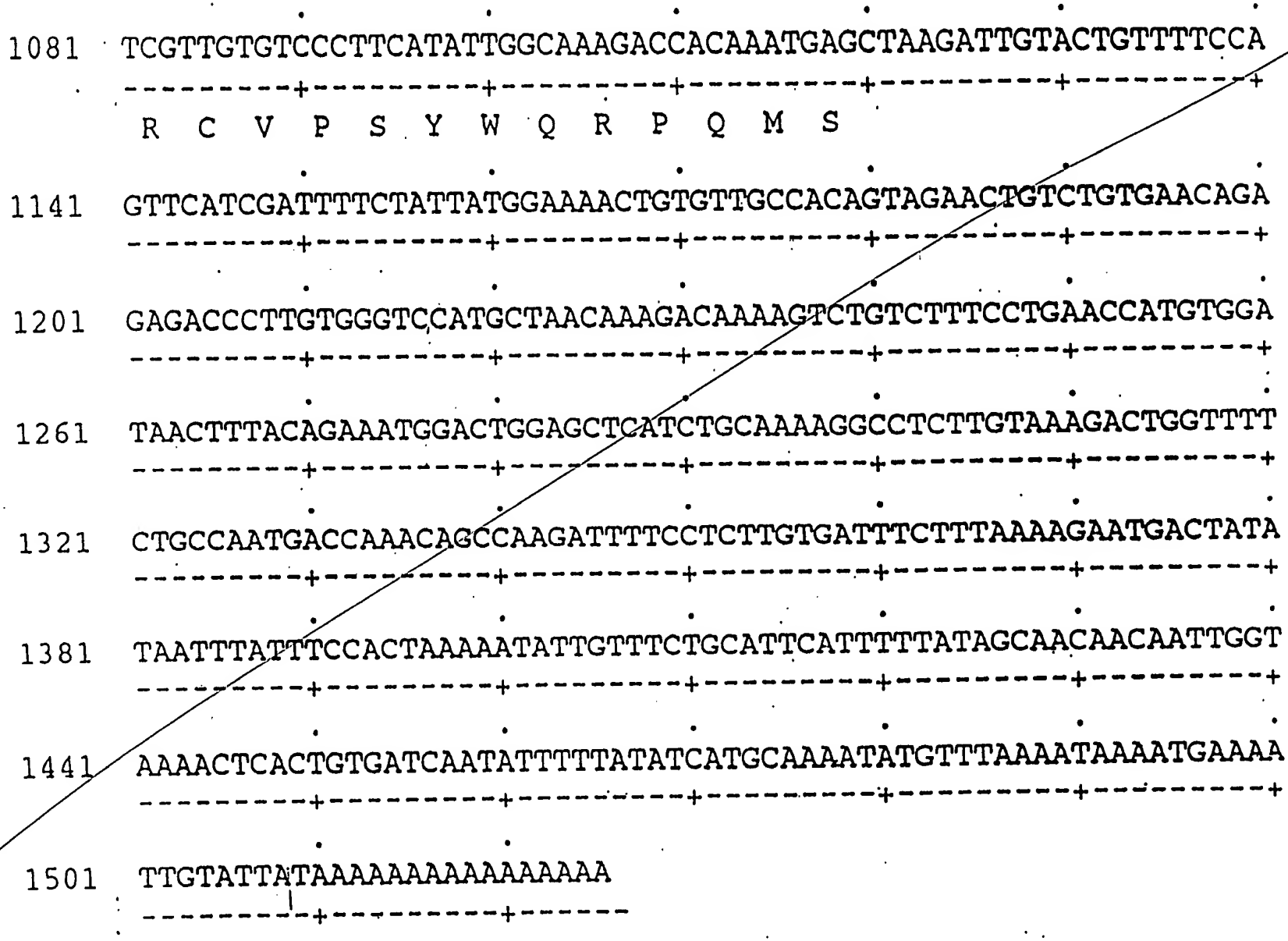

1081 TCGTTGTGTCCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTACTGTTTTCCA
R C V P S Y W Q R P Q M S
1141 GTTCATCGATTTTCTATTATGGAAAACTGTGTTGCCACAGTAGAACTGTCTGTGAACAGA
1201 GAGACCCTTGTGGGTCCATGCTAACAAAGACAAAAGTCTGTCTTTCCTGAACCATGTGGA
1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCTCTTGTAAAGACTGGTTTT
1321 CTGCCAATGACCAAACAGCCAAGATTTTCCTCTTGTGATTTCTTTAAAAGAATGACTATA
1381 TAATTTATTTCCACTAAAAATATTGTTTCTGCATTCATTTTTATAGCAACAACAATTGGT
1441 AAAACTCACTGTGATCAATATTTTTATATCATGCAAAATATGTTTAAAATAAAATGAAAA
1501 TTGTATTATAAAAAAAAAAAAAAA

FIG. 2D

```
           1                                                  50
Pdgfa    .MRTLACLLL LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE
Pdgfb    MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH
 Vegf    .....MNFLL SWVHWSLALL LY........ .......... .LHHAKWSQA
Vegf2    .......MTV LYPEYWKMYK CQ........ .......... .LRKGGWQHN

         51                                                  100
Pdgfa    IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP
Pdgfb    GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
 Vegf    APMAE..... ......GGGQ NHHEVVKFMD .VYQR..... ..........
Vegf2    REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK..... ..........

         101                                                 150
Pdgfa    AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS
Pdgfb    AECKTRTEVF EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT
 Vegf    SYCHPIETLV DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT
Vegf2    TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

         151                                                 200
Pdgfa    RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECAC.... AT........
Pdgfb    QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACKC.... ETVAAARPVT
 Vegf    EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2    STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII
```

FIG. 3A

```
       201                                                    250
Pdgfa  ....TSLNPD YREEDTDVR. .......... .......... ..........
Pdgfb  RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK GKHRKFKHTH DKTALKETLG
 Vegf  RGK....... .GKGQKRKRK KSRYKSWSVY VGARCCLMPW SLPGPHP...
Vegf2  RRSLPATLPQ CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG

       251                                                    300
Pdgfa  .......... .......... .......... .......... ..........
Pdgfb  A......... .......... .......... .......... ..........
 Vegf  ....CGP... .......... .......CSE RRKHLFVQDP QTCKCSCKNT
Vegf2  FHDICGPNKE LDEETCQCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK

       301                                                    350
Pdgfa  .......... .......... .......... .......... ..........
Pdgfb  .......... .......... .......... .......... ..........
 Vegf  ..DSRCKARQ LELNERTCRC DKPRR..... .......... ..........
Vegf2  LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPQKCLL

       351                                                 398
Pdgfa  .......... .......... .......... .......... ........
Pdgfb  .......... .......... .......... .......... ........
 Vegf  .......... .......... .......... .......... ........
Vegf2  KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPQMS
```

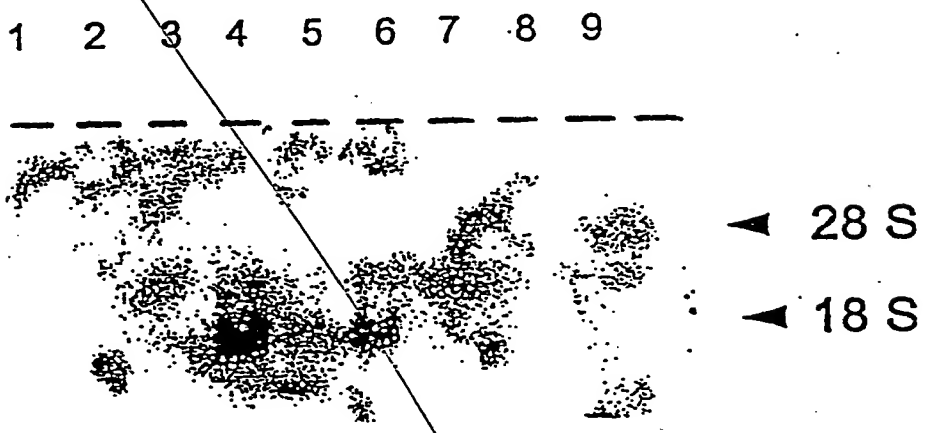
FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLWING TABLE

	PDGFα	PDGFβ	VEGF	VEGF2
PDGFα				
PDGFβ	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

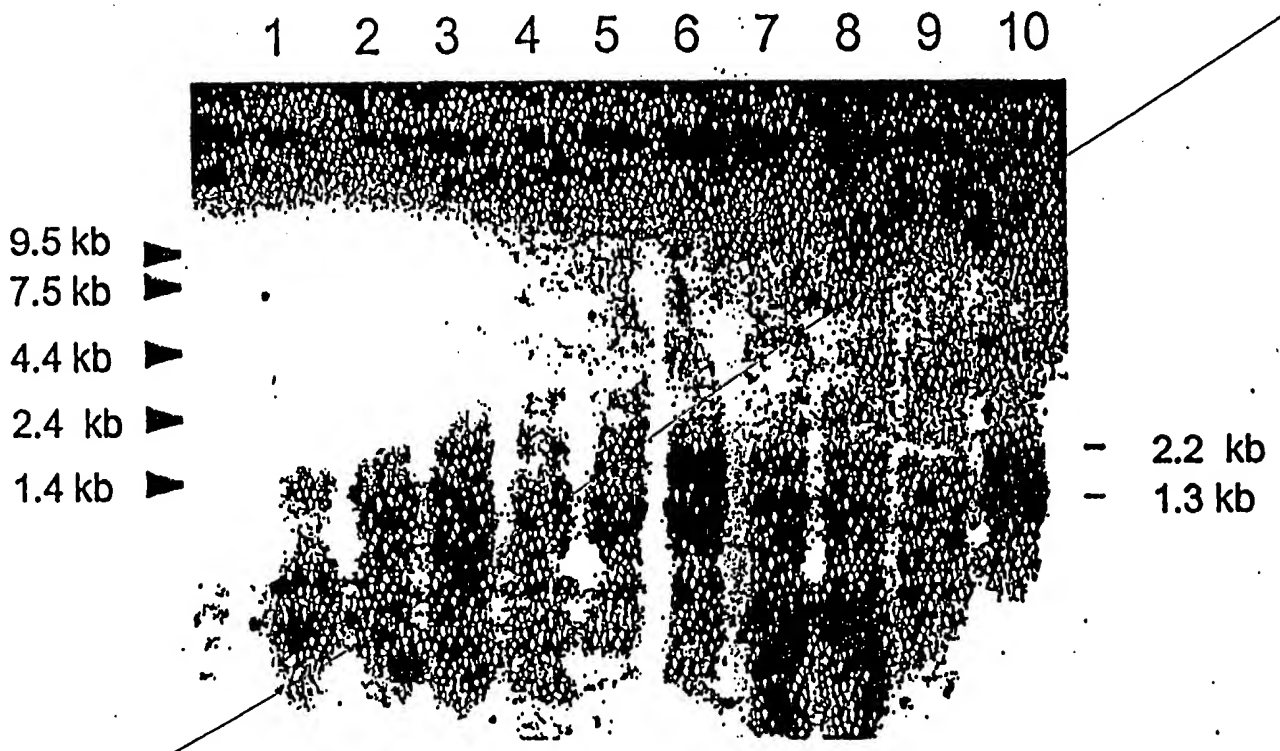
FIG. 4

Expression of VEGF2 mRNA in Human Breast Tumor Cells



1. normal breast tissue
2. breast tumor tissue
3-9. breast tumor cell lines.

FIG. 5

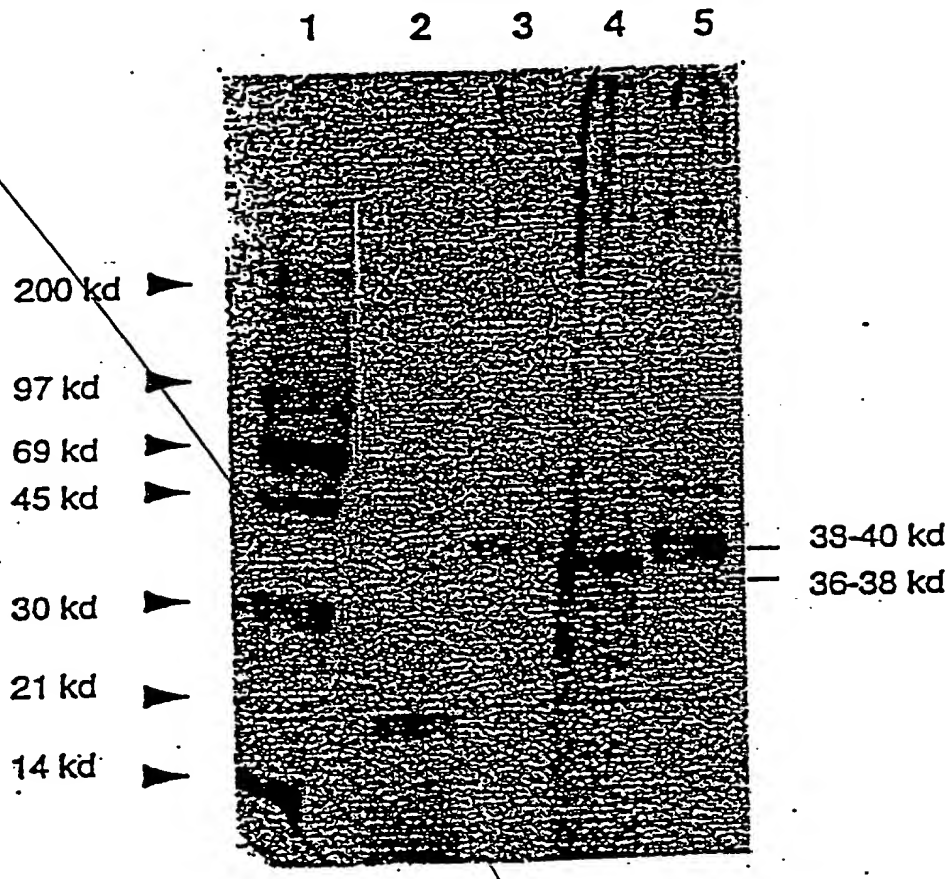


1.	ovary	6.	lung
2.	testes	7.	spleen
3.	gall bladder	8.	prostate
4.	kidney	9.	Hippocampus
5.	liver	10.	heart

Expression of VEGF2 mRNA in human adult tissues.

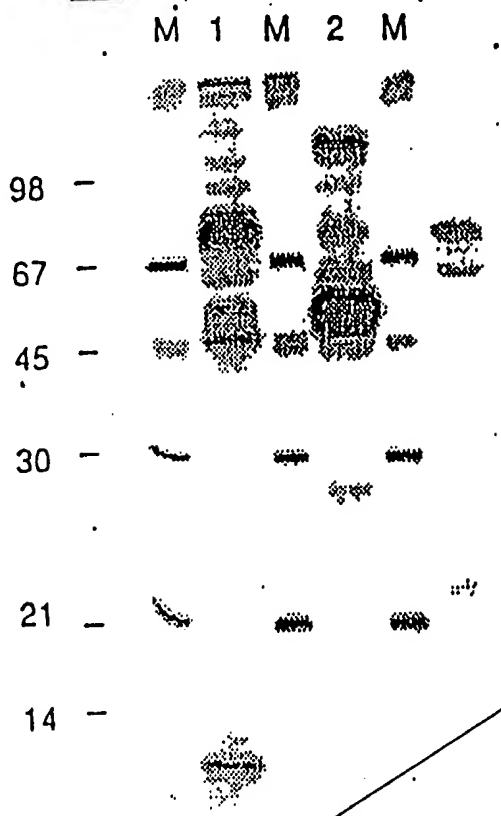
FIG. 6

FIG. 7



Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse & forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

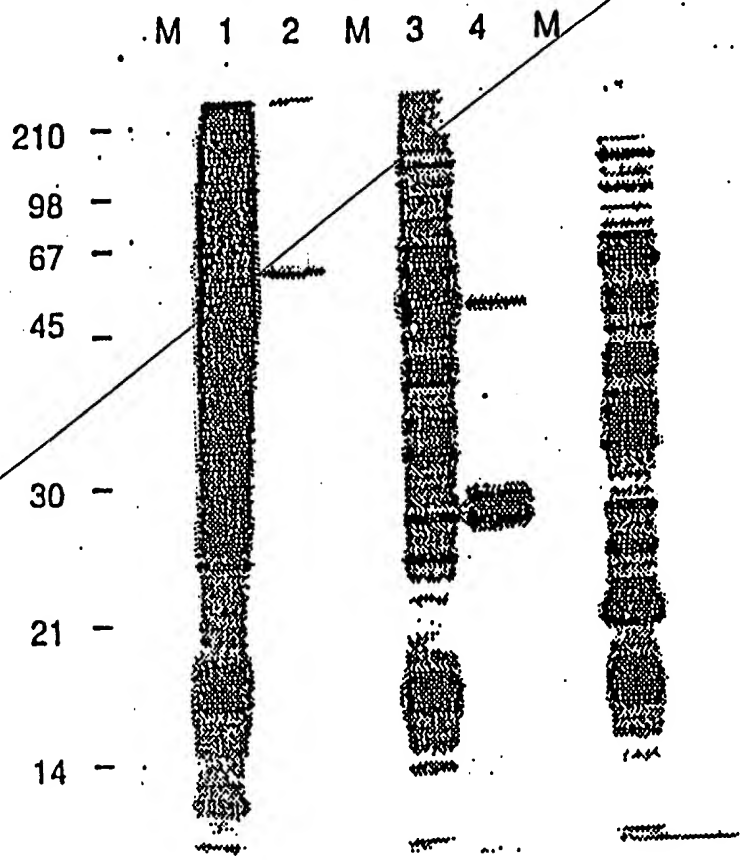
non-reducing gel



Lane M: Marker
Lane 1: vector medium
Lane 2: VEGF2 medium

FIG. 8A

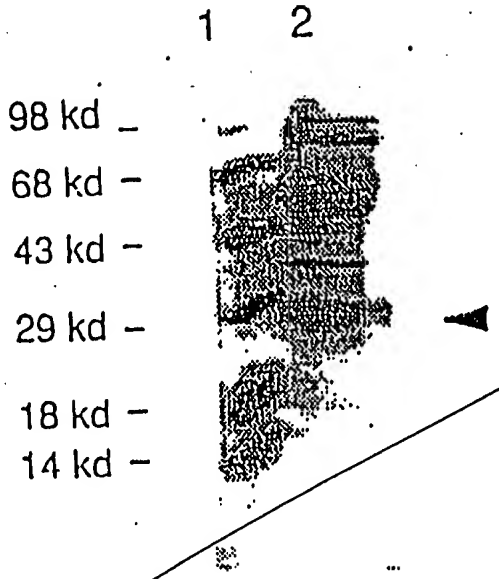
reducing gel



Lane M: Marker
Lane 1: vector cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 cytoplasm
Lane 4: VEGF2 medium

FIG. 8B

FIG. 9



Lane 1: Molelular weight marker
Lane 2. Precipitates containing VEGF2.

FIG. 10

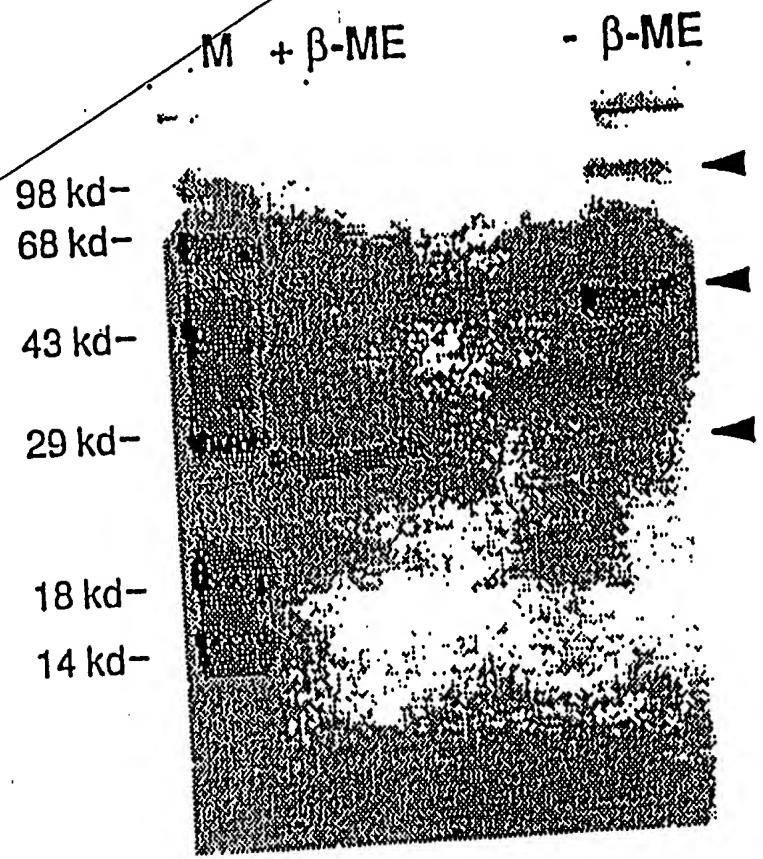
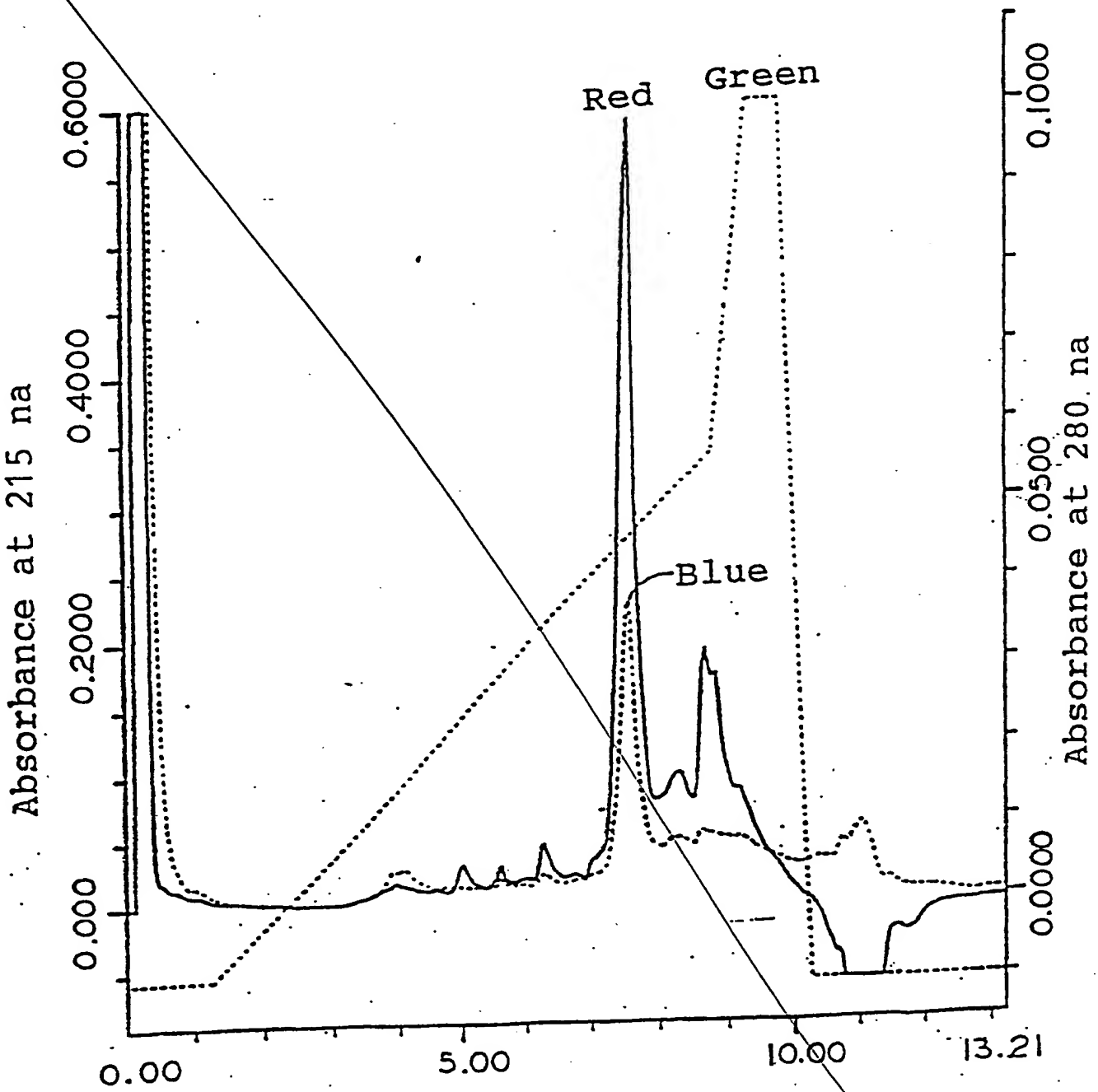


FIG. 11


Red
Green
Blue
Absorbance at 215 na
0.6000
0.4000
0.2000
0.000
Absorbance at 280 na
0.1000
0.0500
0.0000
0.00
5.00
10.00
13.21

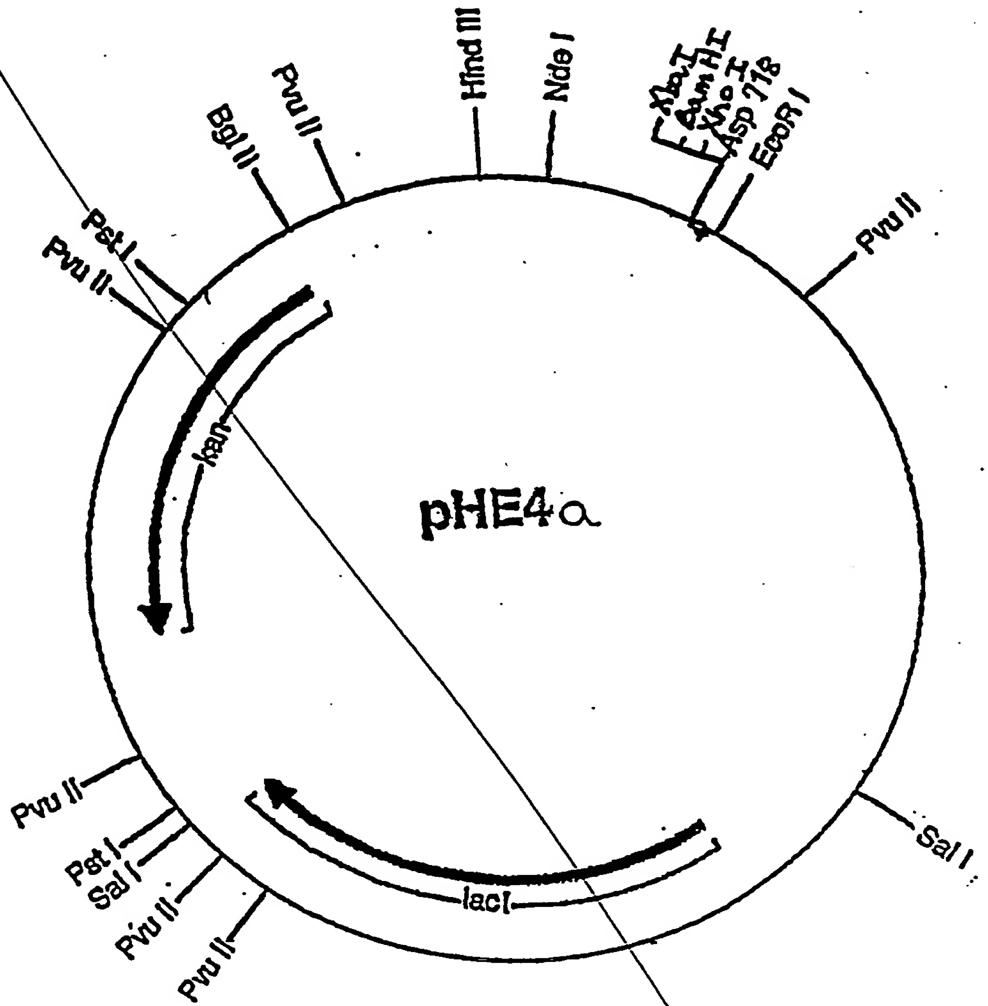
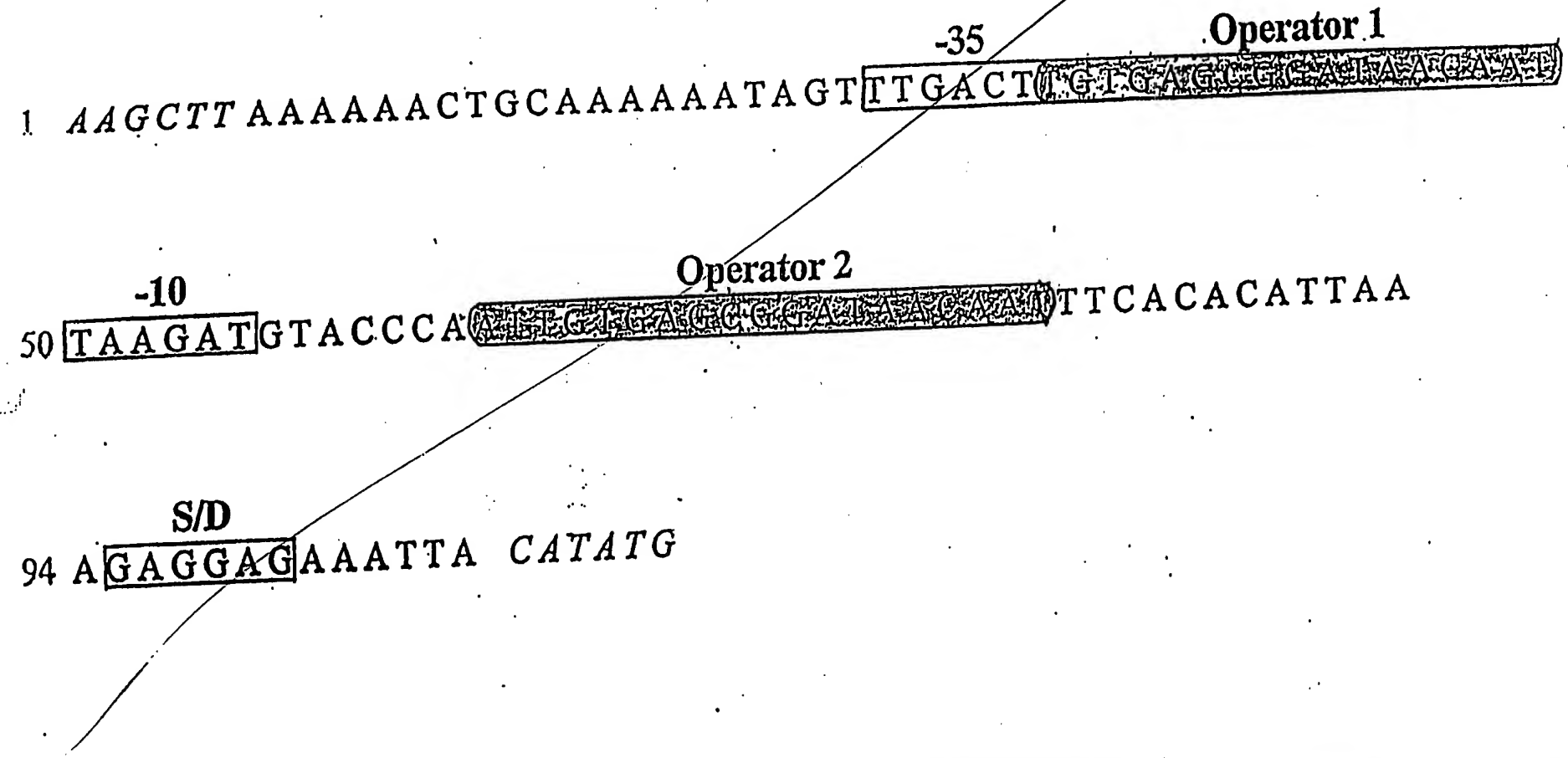

Hind III
Nde I
Pvu II
Bgl II
Xba I
BamHI
Xho I
Asp 718
EcoR I
Pvu II
Pst I
Pvu II
kan
pHE4a
Pvu II
Pst I
Sal I
Pvu II
Pvu II
lacI
Sal I

FIG. 12

FIG. 13


-35
Operator 1
1 AAGCTT AAAAAACTGCAAAAAATAGT TTGACT
-10
Operator 2
50 TAAGAT GTACCCA TTCACACATTAA
S/D
94 A GAGGAG AAATTA CATATG

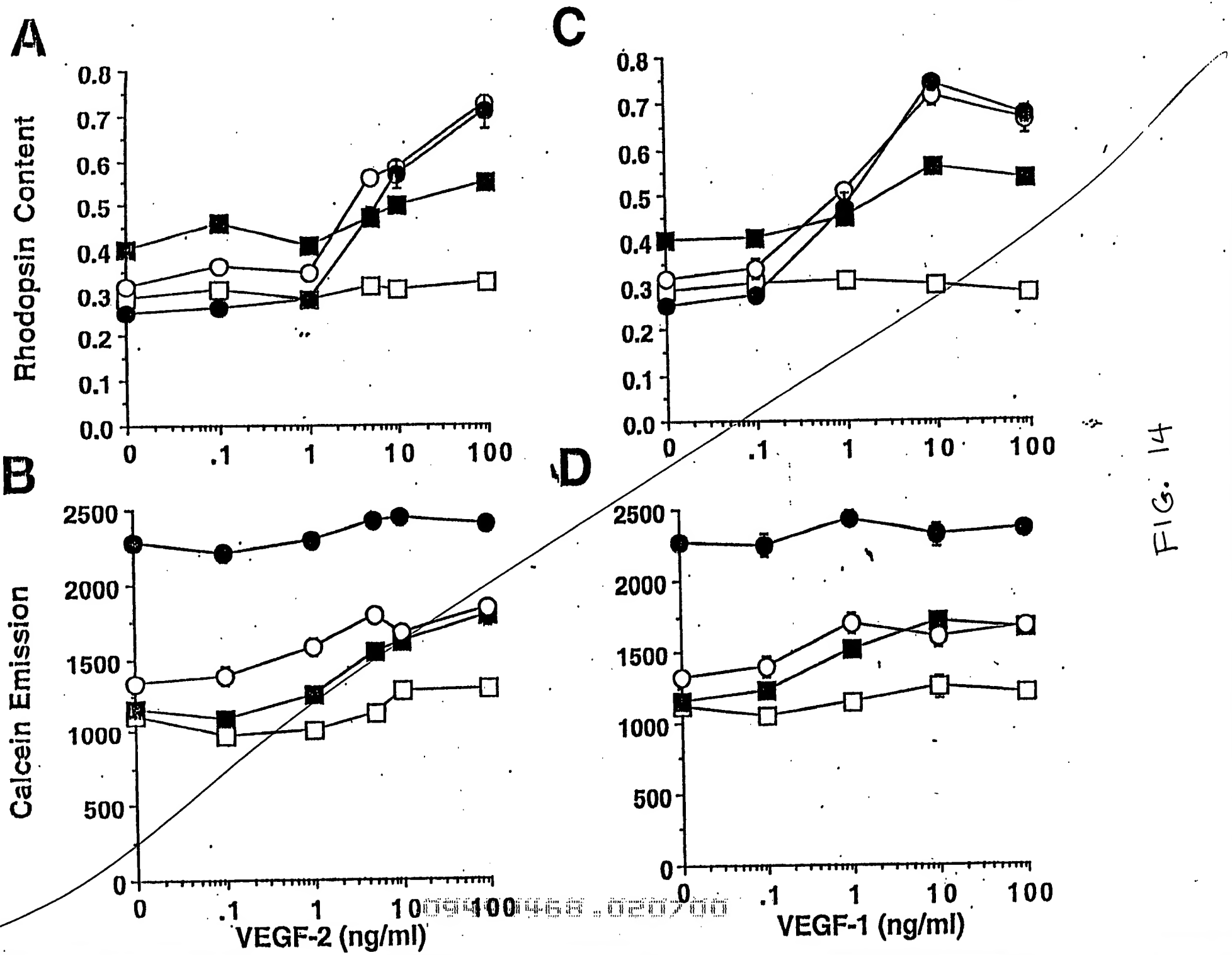

A
Rhodopsin Content
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0
.1
1
10
100
C
B
Calcein Emission
2500
2000
1500
1000
500
0
VEGF-2 (ng/ml)
D
VEGF-1 (ng/ml)

FIG. 14

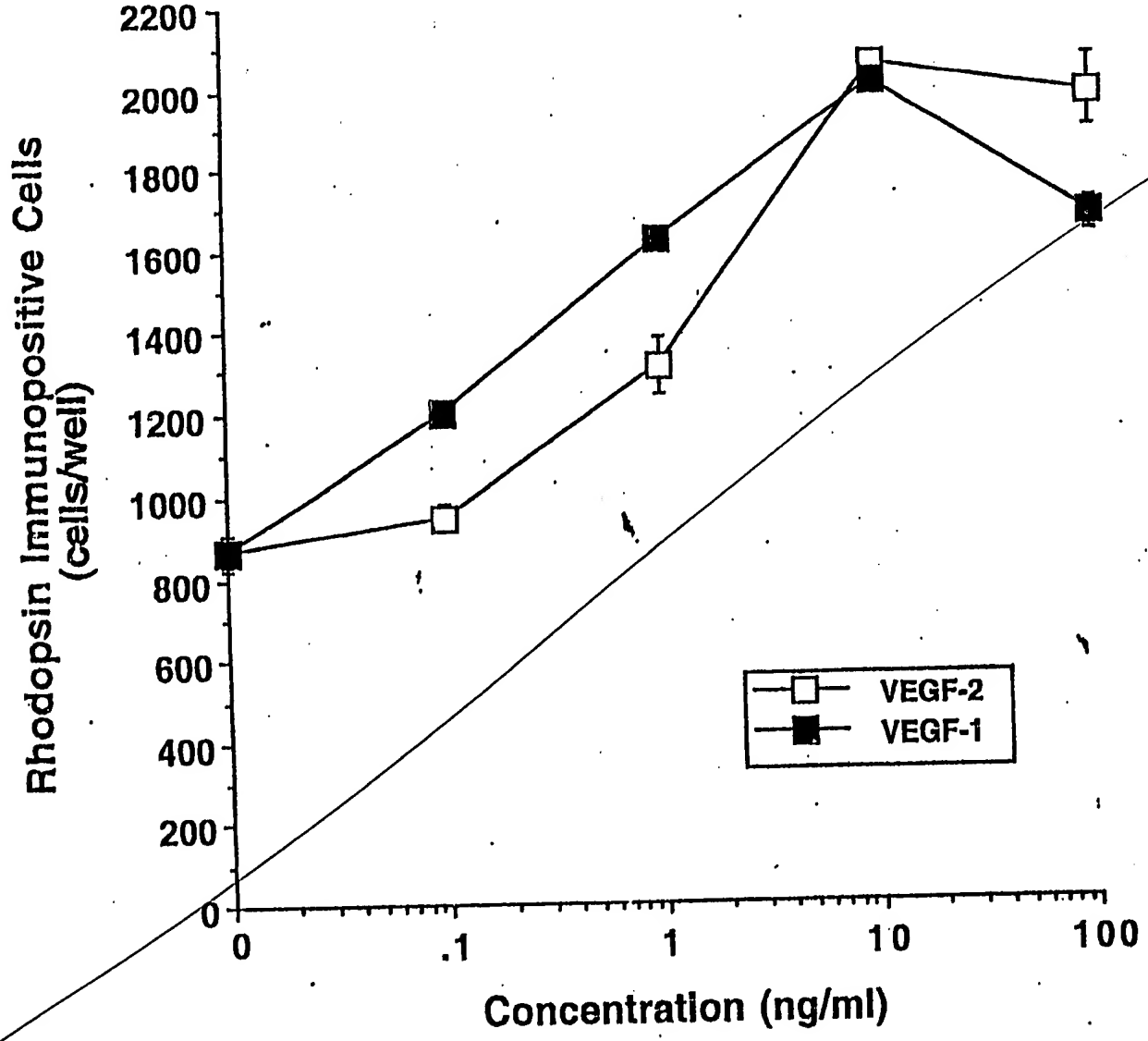


FIG. 15.

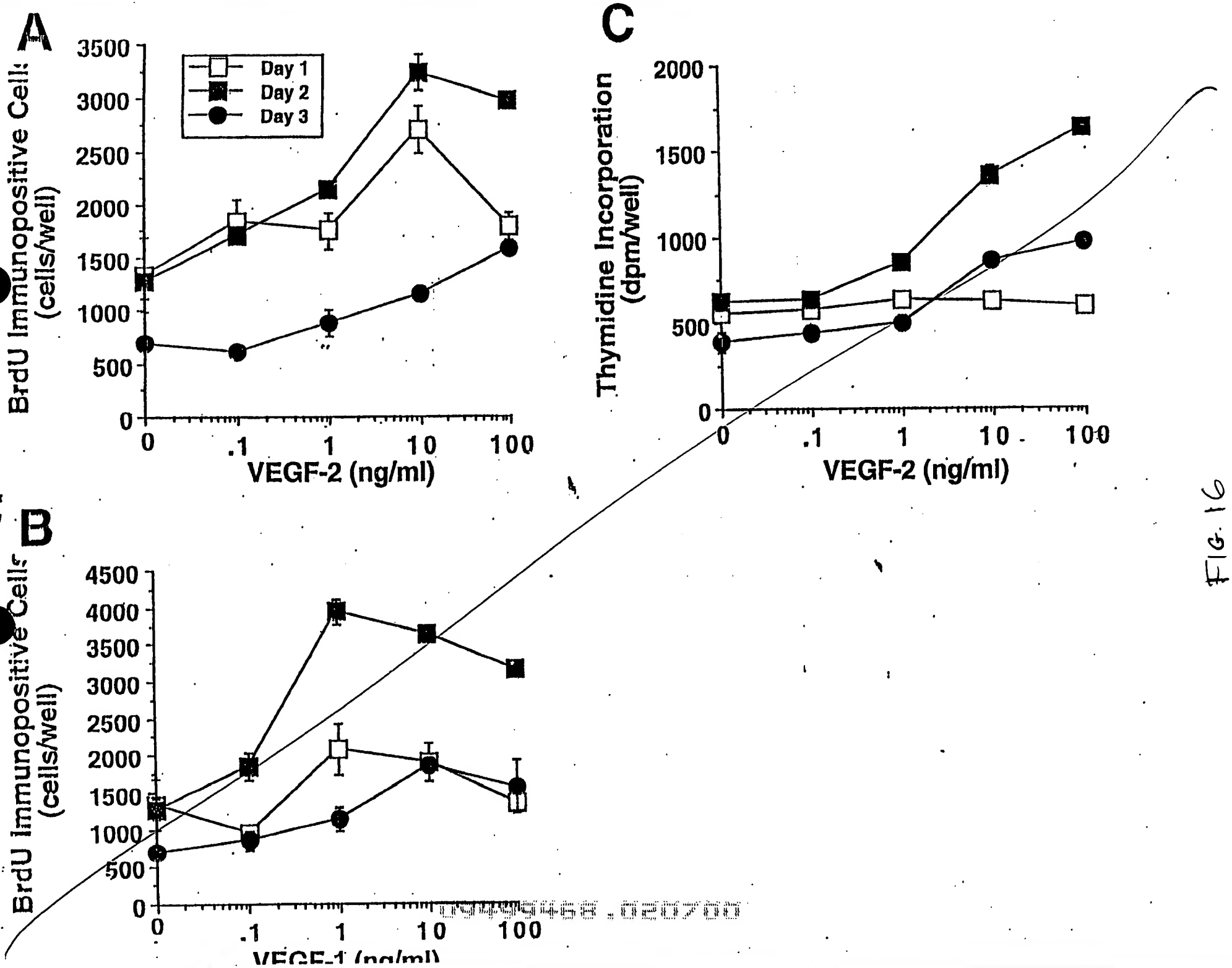

A
BrdU Immunopositive Cells
(cells/well)
3500
3000
2500
2000
1500
1000
500
0
Day 1
Day 2
Day 3
0
.1
1
10
100
VEGF-2 (ng/ml)
C
Thymidine Incorporation
(dpm/well)
2000
1500
1000
500
0
0
.1
1
10
100
VEGF-2 (ng/ml)
B
BrdU Immunopositive Cells
(cells/well)
4500
4000
3500
3000
2500
2000
1500
1000
500
0
0
.1
1
10
100
VEGF-1 (ng/ml)

FIG. 16

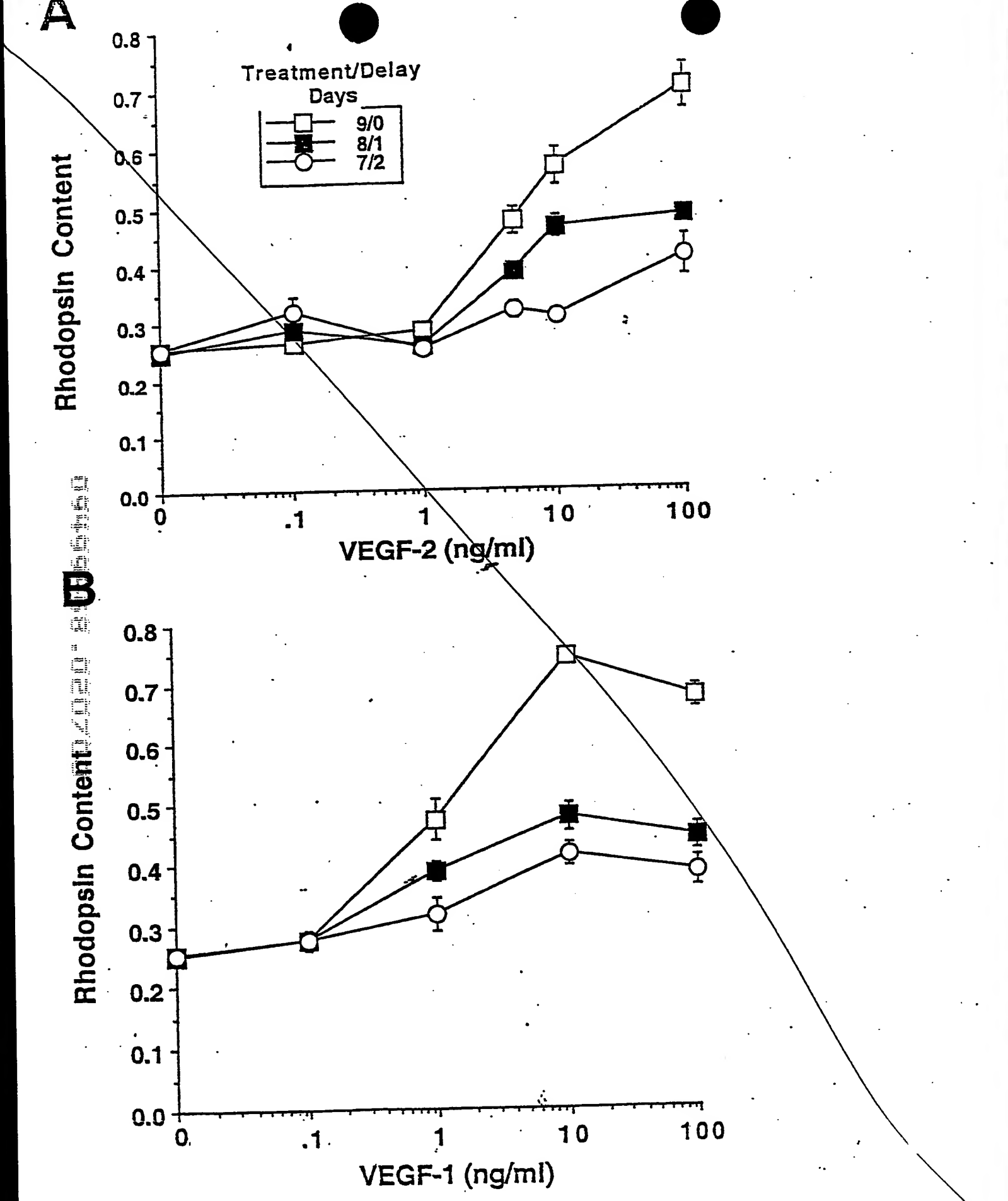

A
Rhodopsin Content
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Treatment/Delay
Days
9/0
8/1
7/2
0
.1
1
10
100
VEGF-2 (ng/ml)
B
Rhodopsin Content
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0
.1
1
10
100
VEGF-1 (ng/ml)

FIG. 17

FIG. 18

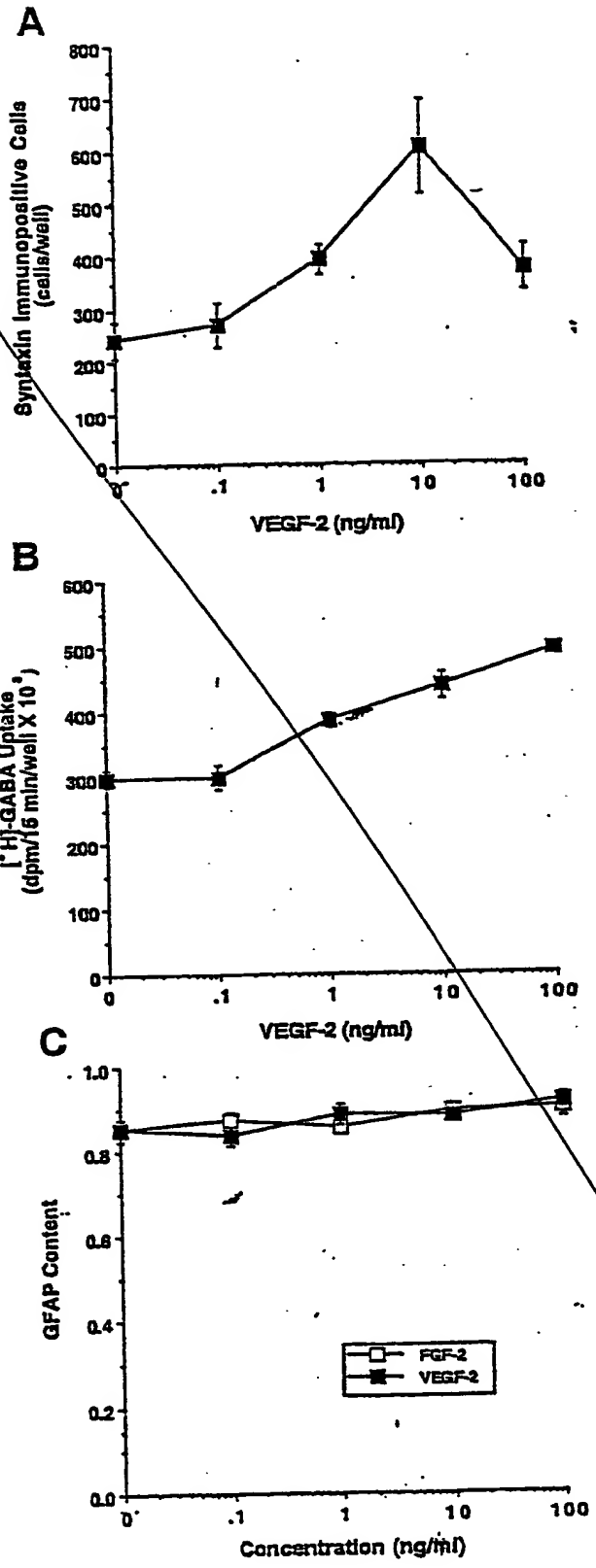

A
Synaptotagmin Immunopositive Cells (cells/well)
800
700
600
500
400
300
200
100
0
0
.1
1
10
100
VEGF-2 (ng/ml)
B
[3H]-GABA Uptake (dpm/15 min/well X 10-3)
600
500
400
300
200
100
0
0
.1
1
10
100
VEGF-2 (ng/ml)
C
GFAP Content
1.0
0.8
0.6
0.4
0.2
0.0
FGF-2
VEGF-2
0
.1
1
10
100
Concentration (ng/ml)

FIG. 19

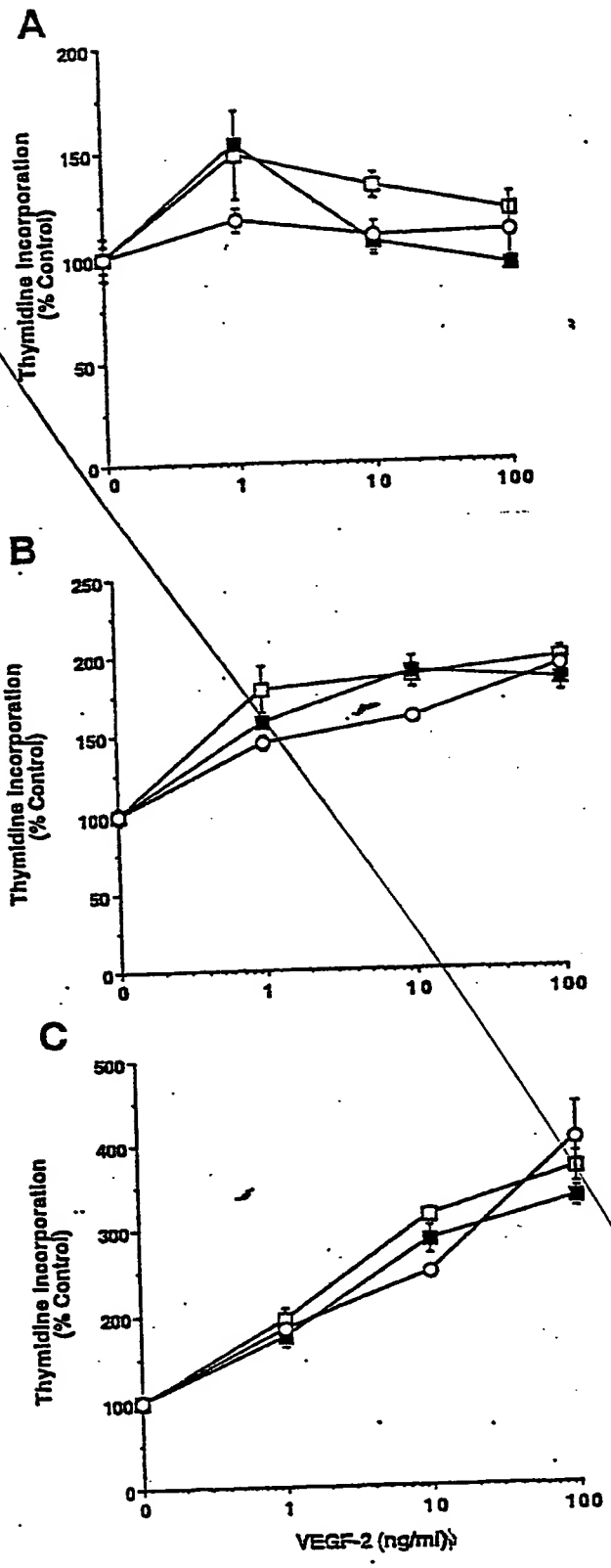

A
B
C
Thymidine Incorporation (% Control)
200
150
100
50
0
250
500
400
300
0
1
10
100
VEGF-2 (ng/ml)

FIG. 20

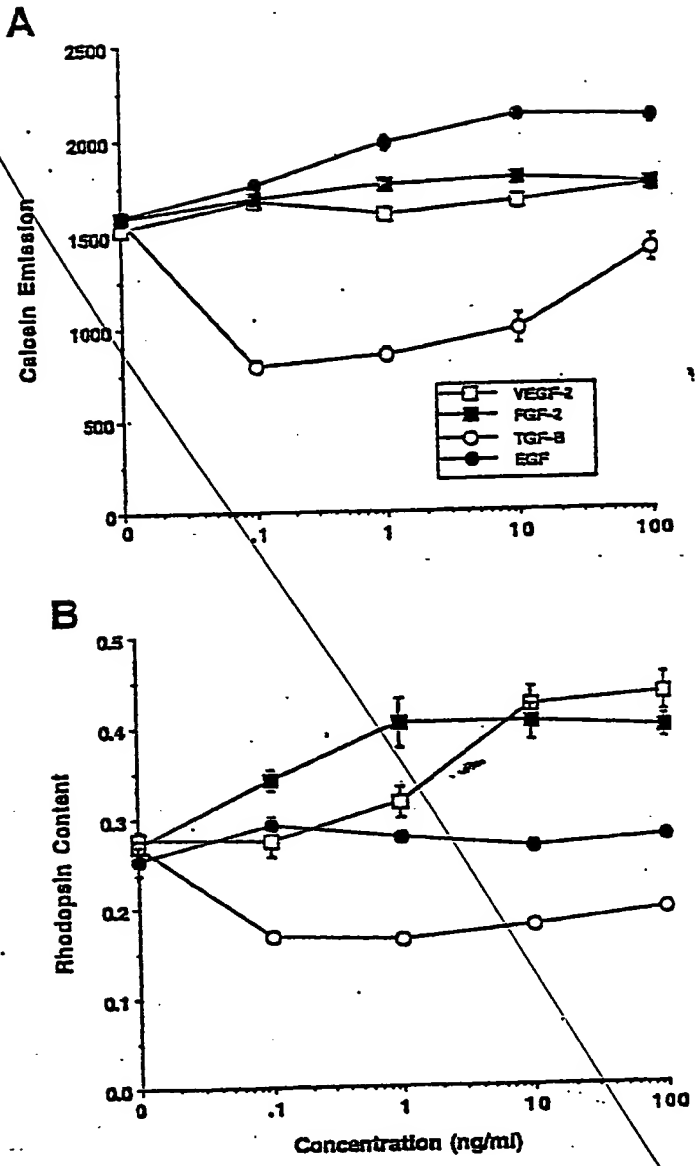

A
Calcein Emission
2500
2000
1500
1000
500
0
0
.1
1
10
100
VEGF-2
FGF-2
TGF-B
EGF
B
Rhodopsin Content
0.5
0.4
0.3
0.2
0.1
0.0
0
.1
1
10
100
Concentration (ng/ml)

FIG. 21

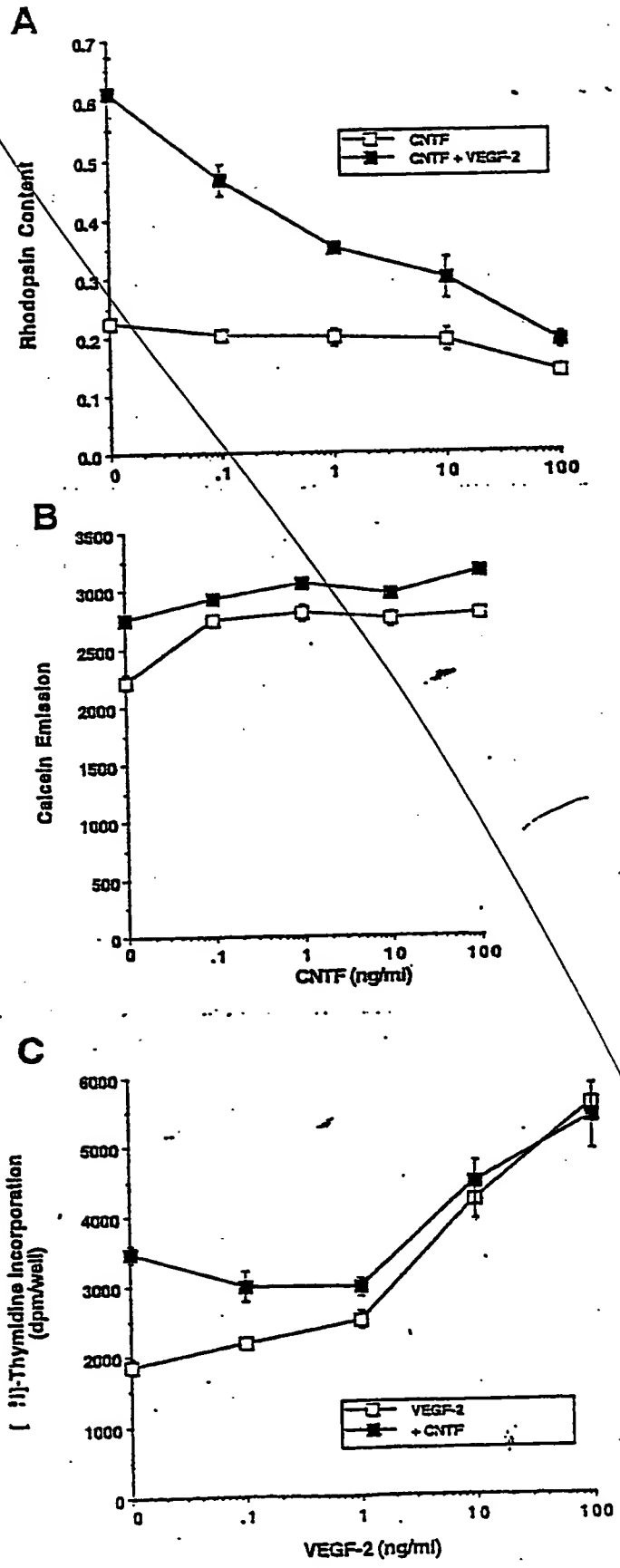
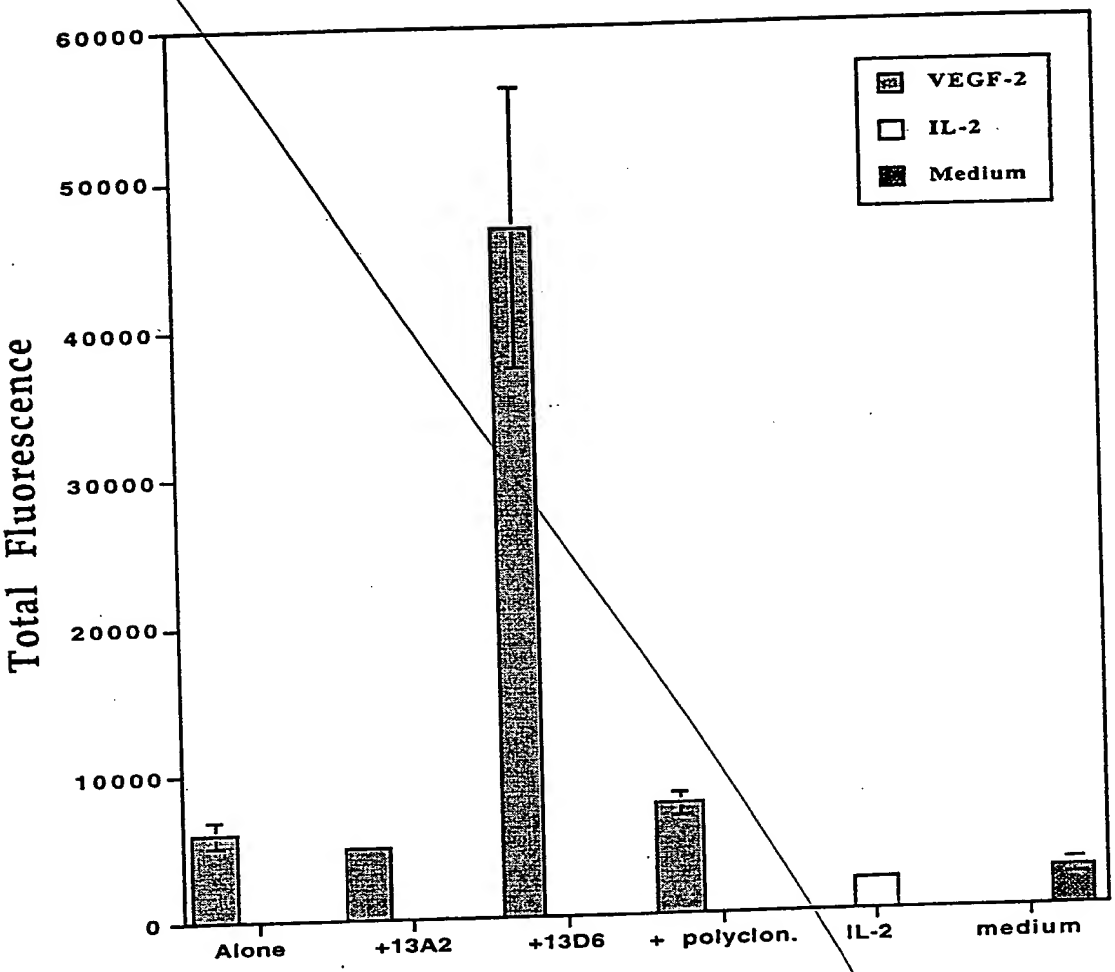

A
Rhodopsin Content
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0
.1
1
10
100
CNTF
CNTF + VEGF-2
B
Calcein Emission
3500
3000
2500
2000
1500
1000
500
0
0
.1
1
10
100
CNTF (ng/ml)
C
[³H]-Thymidine Incorporation (dpm/well)
6000
5000
4000
3000
2000
1000
0
0
.1
1
10
100
VEGF-2 (ng/ml)
VEGF-2
+ CNTF

FIG. 22


60000
50000
40000
30000
20000
10000
0
Total Fluorescence
VEGF-2
IL-2
Medium
Alone
+13A2
+13D6
+ polyclon.
IL-2
medium

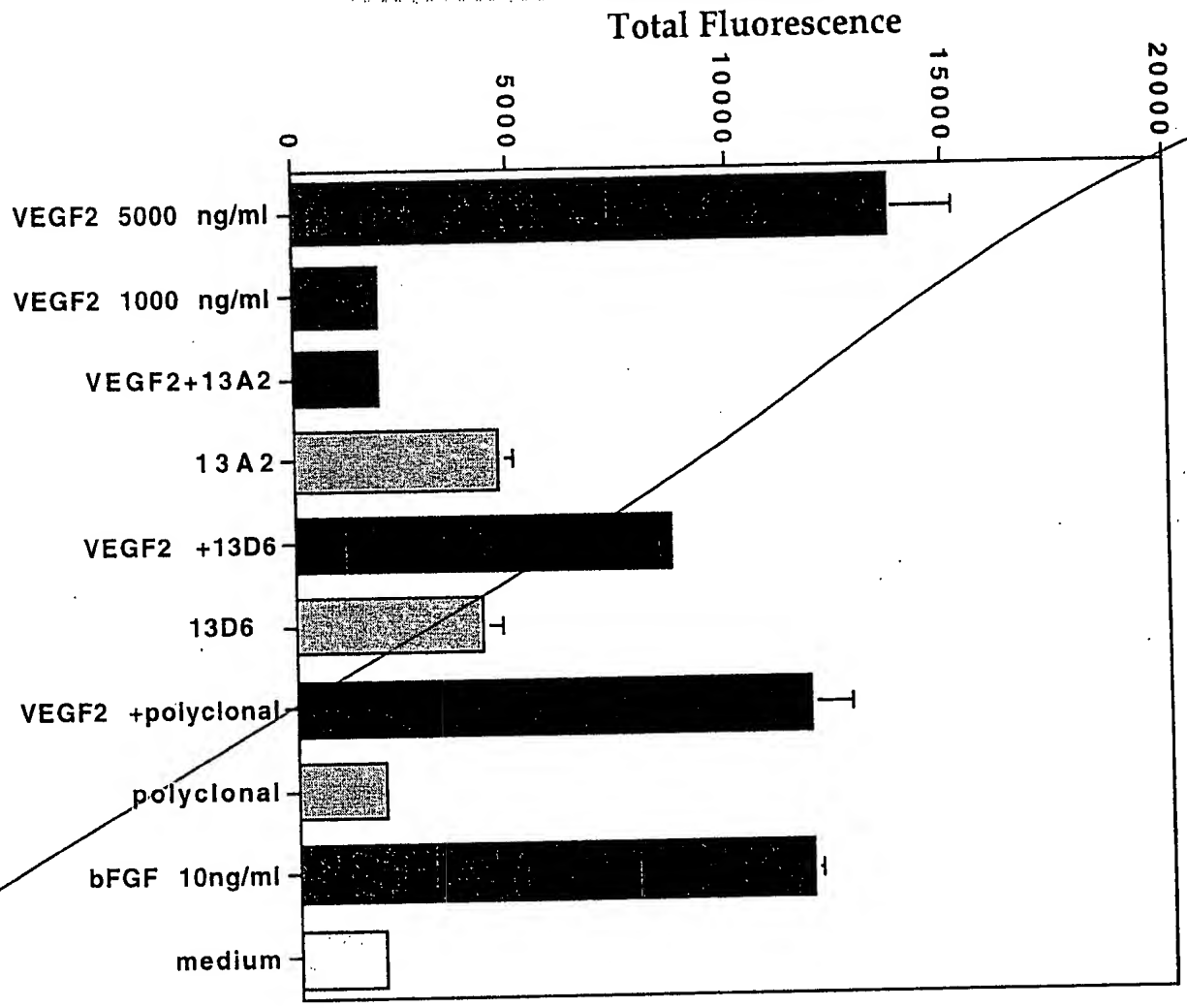

Total Fluorescence
0
5000
10000
15000
20000
VEGF2 5000 ng/ml
VEGF2 1000 ng/ml
VEGF2+13A2
13A2
VEGF2 +13D6
13D6
VEGF2 +polyclonal
polyclonal
bFGF 10ng/ml
medium

FIG.23

FIG. 24

Epitope map for murine anti VEGF-2 MAB

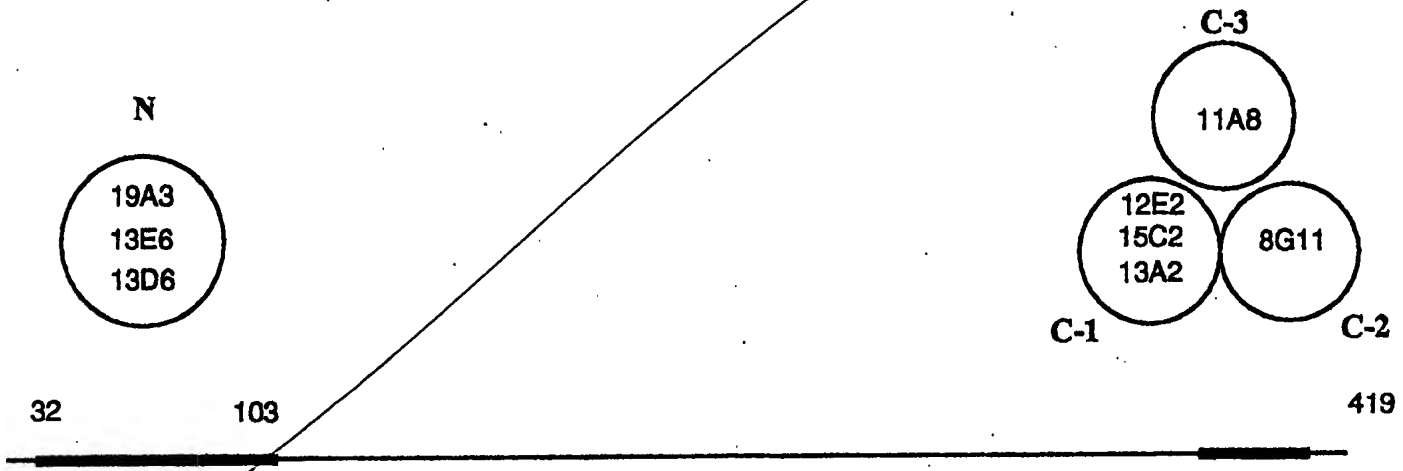


FIG. 25

Murine VEGF-2 MAB status

	Isotype	Rel.affinity ng/ml	Specificity	Reactivity Western	Reactivity ELISA	Purified mg
12E2	γ1	<1	C-1	+	+	27
13A2	γ1	<1	C-1	n.t	+	27
15C2	γ1	<1	C-1	n.t	+	10
13D6	γ1	<1	N	+	+	25
13E6	γ1	1	N	+	+	38
19A3	γ1	1	N	+	+	54
8G11	γ1	5	C-2	+	+	7
11A8	γ1	<1	C-3	+	+	9